

5'-GGCGU <sup>U</sup> CA CACC <sup>U</sup> CCGCUGA GUGG <sup>C</sup> A      G	16S A Site rRNA (SEQ ID NO. 1)
5'-GGCGUCACACC <sup>U</sup> CCGCAG UGUGG <sup>C</sup> A      G	Control RNA (SEQ ID NO. 2)

Figure 1. Sequence and structure of 27mer RNA target

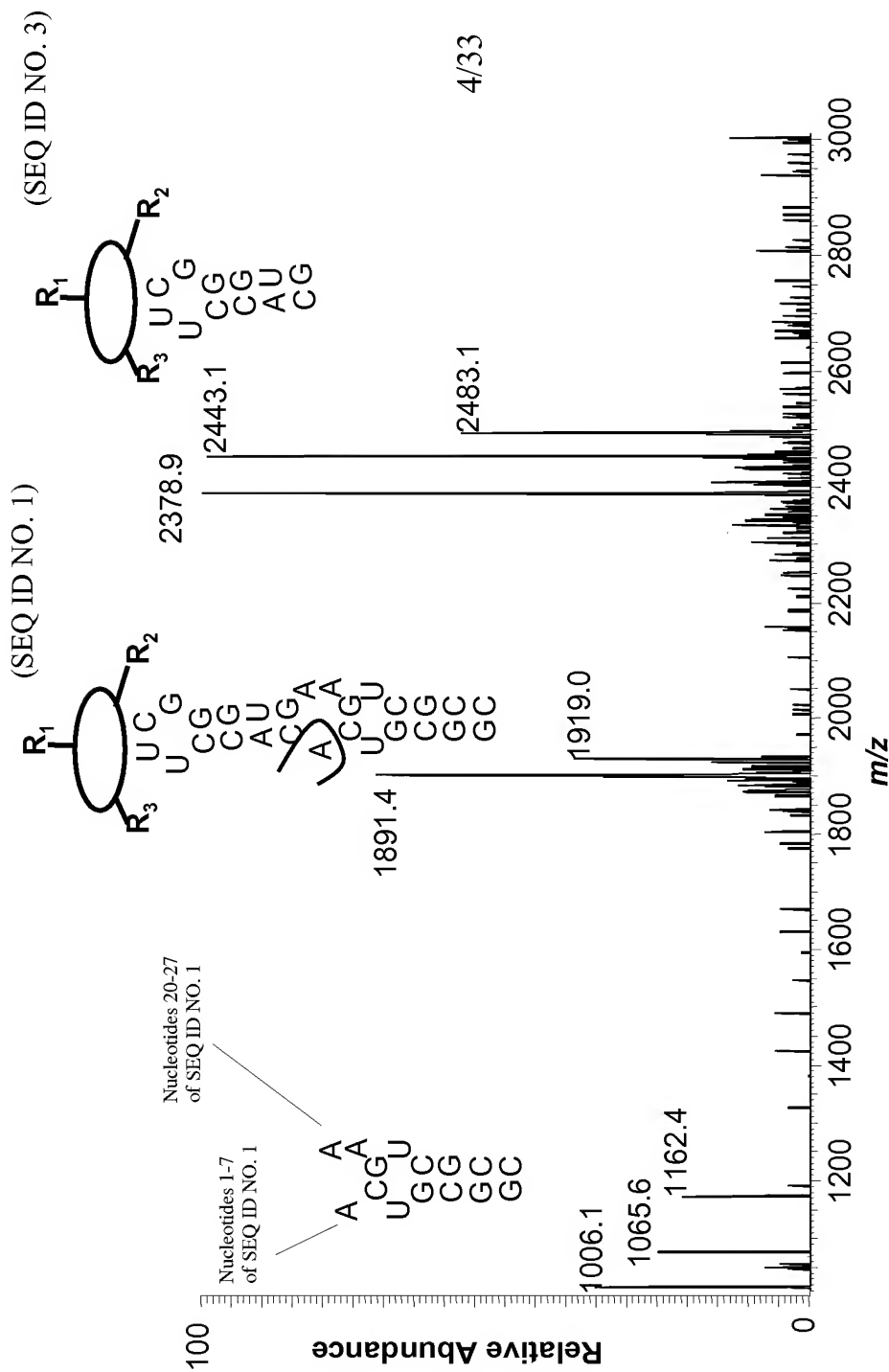


Figure 4. MS\_MS analysis of member bound to RNA/DNA chimera

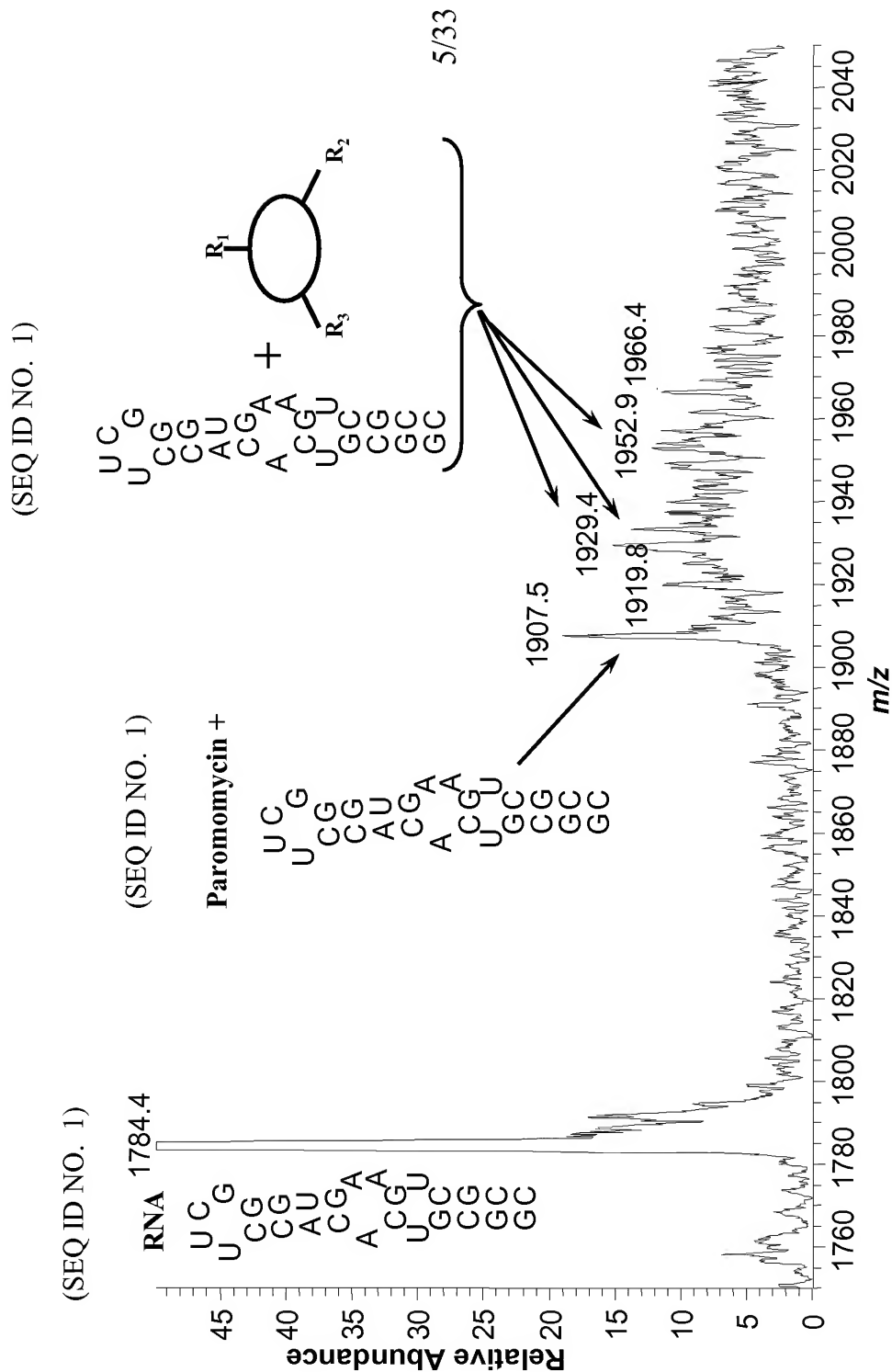


Figure 5. ESI-MS of RNA/DNA chimera bound to paromomycin and library

The figure displays a mass spectrum and an RNA secondary structure diagram. The mass spectrum shows relative abundance versus m/z, with major peaks at 1906.0, 1934.3, 2401.4, 2465.3, and 2506.1. The RNA secondary structure diagram shows a sequence of nucleotides (U, C, G, A) forming a stem-loop structure, with labels R<sub>1</sub>, R<sub>2</sub>, and R<sub>3</sub> indicating specific regions.

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Figure 7. MS-MS analysis of member bound to RNA/DNA chimera at the A-Site



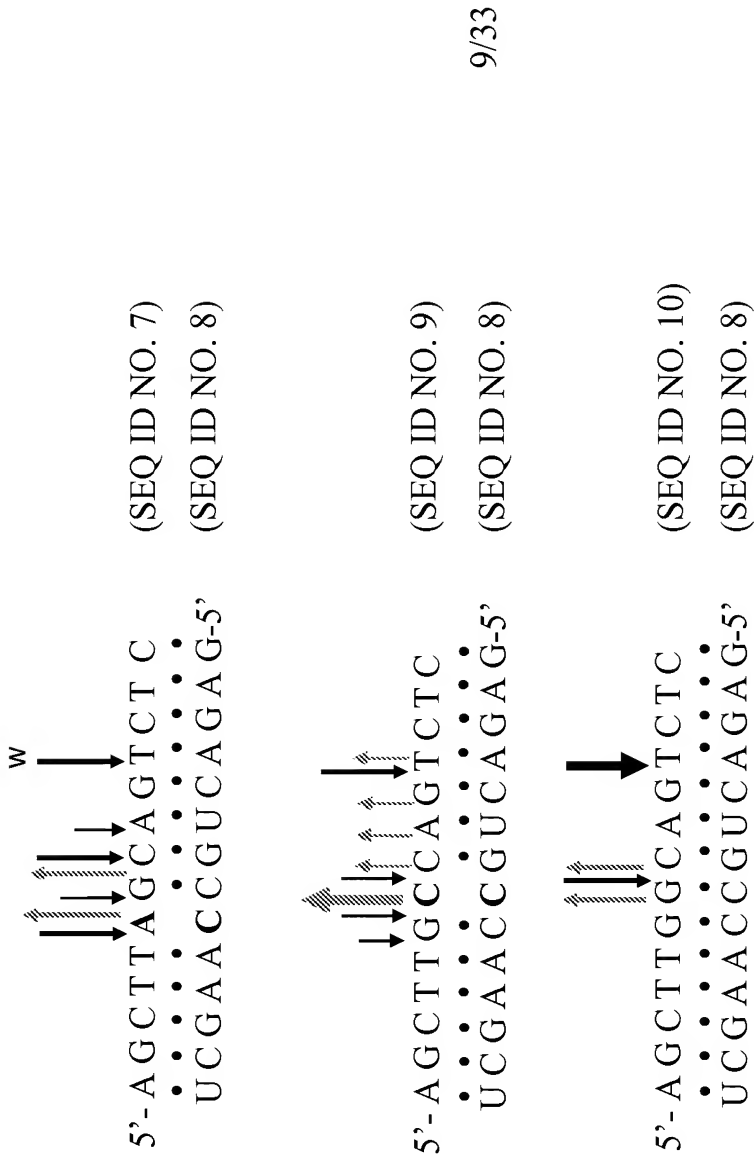


Figure 9. MS Fragmentation of DNA:RNA duplexes

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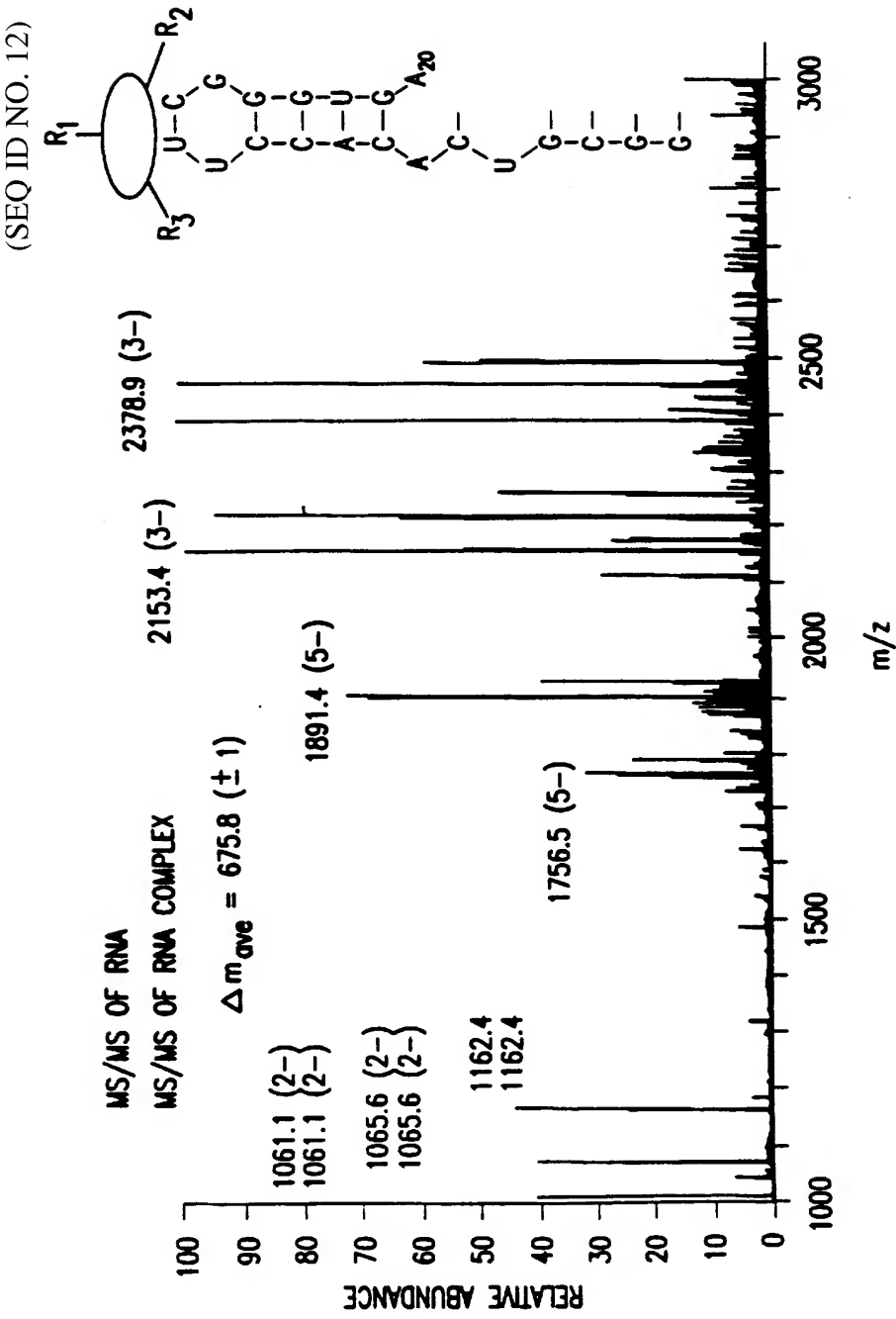


Figure 10

(SEQ ID NO. 1)





# **MASS analysis of 16S A site RNA plus 216 member library (performed on quadrupole ion trap)**

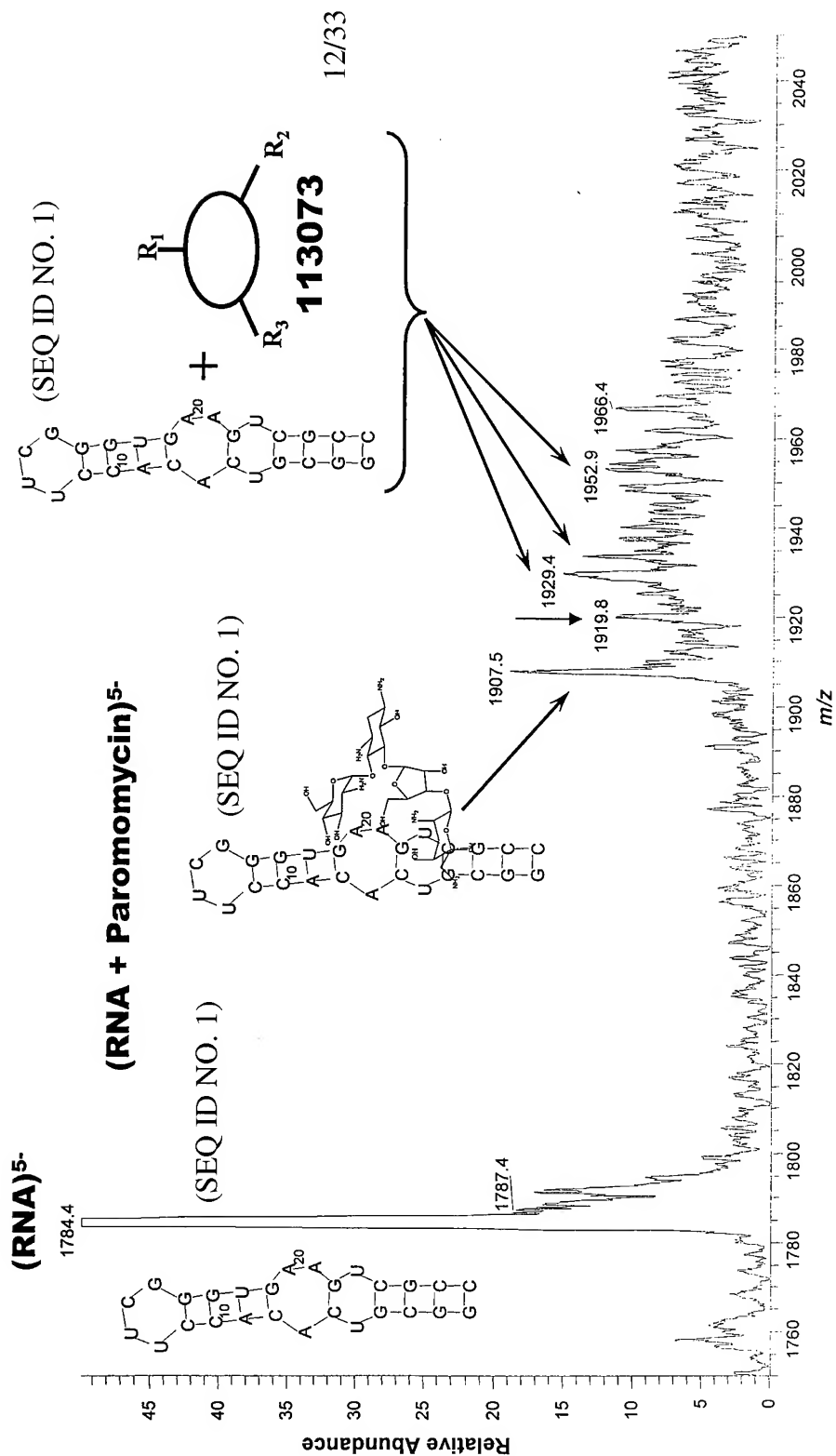


Figure 12

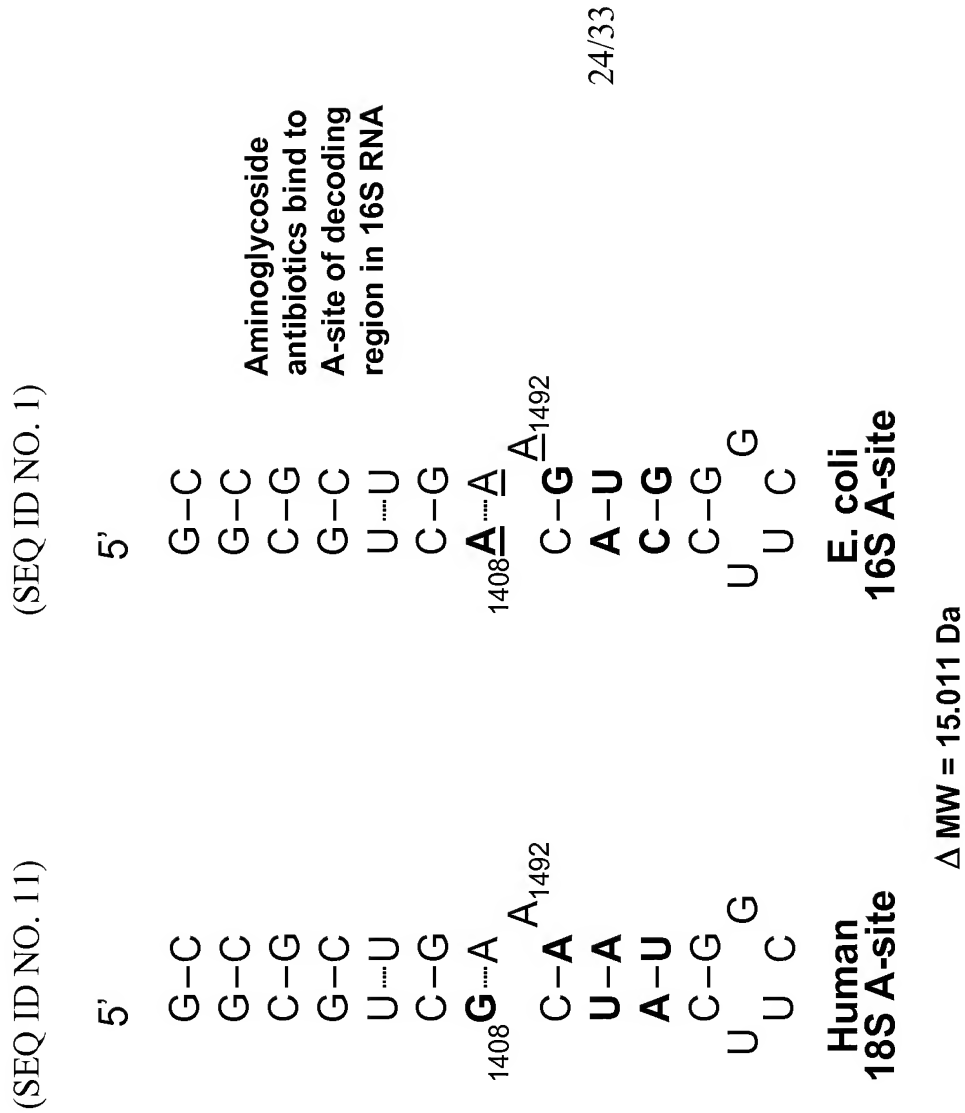


Figure 24. Eukaryotic and Prokaryotic A-Sites

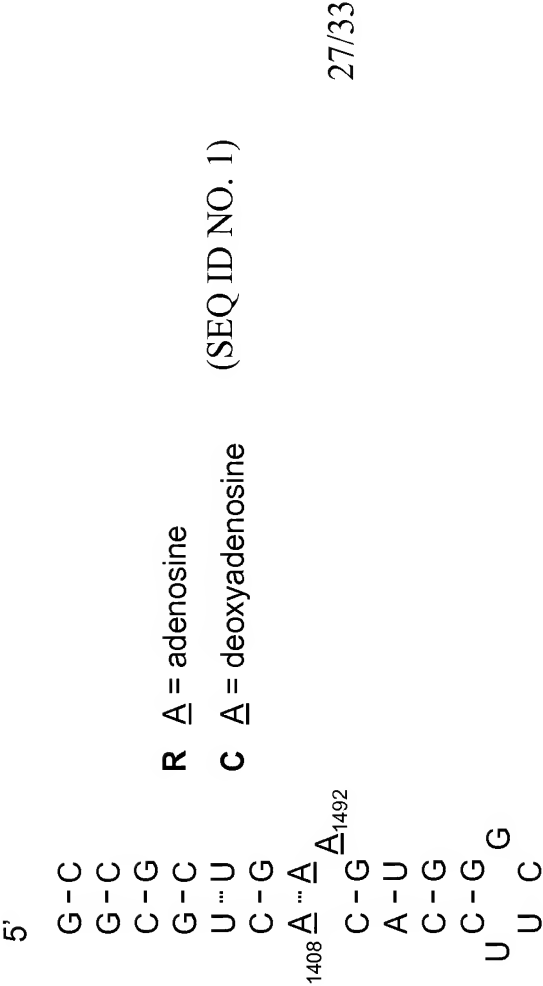


Figure 27